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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 19 17:34:09 EDT 2007

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Reviewer Comments:

<150>

<151>

Please remove the above numeric identifiers, since no prior application information is given.

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide

metAfw

Please move the "metAfw" over to the left, one space away from "Oligonucleotide."

<210> 6

<211> 42 n=1:1:1:1 mixture of A,T,C and G.

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

GAPDHrevII

<400> 6

gaccttaatt aagatctcat atgttccacc agctatttgt ta

42

The <211> response shows invalid information: do not show explanatory information on the <211> line; it belongs in the <220>-<223> section. Also, no "n's" appear in the sequence. Same type of error in Sequences 10 and 12: no "n's" in those sequences, although an explanation appears.

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

metAmutfw1

<400> 9

nnncagatca cgccatacga tctac

25

The "n's" in the above sequence are not explained. Please explain them in the <220>-<223> section. Same type of error in Sequence 11.

Application No: 10530843 Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-19 16:47:51.252
 Finished: 2007-06-19 16:47:52.739
 Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 487 ms
 Total Warnings: 10
 Total Errors: 10
 No. of SeqIDs Defined: 12
 Actual SeqID Count: 12

Error code	Error Description
E 201	Mandatory field data missing in <140>
E 201	Mandatory field data missing in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 202	Invalid input format; Value must be an integer in <211> in SEQ ID
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 253	The number of bases differs from <211> Input: 0 Calculated:42
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 342	'n' position not defined found at POS: 1 SEQID(9)
E 342	'n' position not defined found at POS: 2 SEQID(9)
E 342	'n' position not defined found at POS: 3 SEQID(9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 342	'n' position not defined found at POS: 1 SEQID(11)
E 342	'n' position not defined found at POS: 2 SEQID(11)
E 342	'n' position not defined found at POS: 3 SEQID(11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

SEQUENCE LISTING

<110> Consortium fuer elektrochemische Industrie GmbH

<120> Feedback-resistant Homoserine-Transsuccinylases

<130> CO-P#####

<140> 10530843

<141> 2007-06-19

<150>

<151>

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(930)

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<305> 5331

<306> 1453-1474

<307> 1997

<400> 1

atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt 48

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1 5 10 15

gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa 96

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu

20 25 30

att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att 144

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile

35 40 45

gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag 192

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln

50 55 60

gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg 240

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr

65 70 75 80

ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag	288
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln	
85 90 95	
gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg	336
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu	
100 105 110	
gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg	384
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu	
115 120 125	
gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg	432
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala	
130 135 140	
gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc	480
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg	
145 150 155 160	
acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat	528
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His	
165 170 175	
gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg	576
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser	
180 185 190	
cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg	624
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu	
195 200 205	
gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt	672
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser	
210 215 220	
aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg	720
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala	
225 230 235 240	
caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac	768
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp	
245 250 255	
ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca	816
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr	
260 265 270	
ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg	864
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp	
275 280 285	
ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg	912
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met	
290 295 300	
aat cca acg ctg gat taa	930

Asn Pro Thr Leu Asp

305

<210> 2

<211> 309

<212> PRT

<213> Escherichia coli

<400> 2

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
1 5 10 15

Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
20 25 30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
35 40 45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
50 55 60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
65 70 75 80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
85 90 95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
100 105 110

Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
115 120 125

Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
130 135 140

Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
145 150 155 160

Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
165 170 175

Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
180 185 190

Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
195 200 205

Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
210 215 220

Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
225 230 235 240

Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
245 250 255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
260 265 270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
275 280 285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
290 295 300

Asn Pro Thr Leu Asp
305

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide metAfw

<400> 3

gateccatgg ctctcttttag tcattcttat 30

<210> 4

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

metArev

<400> 4

gatcgagctc agtactatta atccagcggt ggattc 36

<210> 5

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

GAPDHfw

<400> 5

gtcgagcgt gaggcgagtc agtcgcgtaa tgc 33

<210> 6

<211> 42 n=1:1:1:1 mixture of A,T,C and G.

